

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/385,229DATE: 04/12/95
TIME: 12:39:53

INPUT SET: S1922.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Jacobs, Cindy A.
Smith, Craig A.(ii) TITLE OF INVENTION: Method of Treating TNF-Dependent
Inflammation Using Tumor Necrosis Factor Antagonists

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: U.S.A.
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/385,229
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/07/946,236
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wight, Christopher L.
(B) REGISTRATION NUMBER: 31,680
(C) REFERENCE/DOCKET NUMBER: 2503

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 587-0606

(2) INFORMATION FOR SEQ ID NO:1:

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/385,229DATE: 04/12/95
TIME: 12:40:04

INPUT SET: S1922.raw

47
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 1641 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: single
52 (D) TOPOLOGY: linear
53
54 (ii) MOLECULE TYPE: cDNA
55
56 (iii) HYPOTHETICAL: NO
57
58 (iv) ANTI-SENSE: NO
59
60 (vi) ORIGINAL SOURCE:
61 (A) ORGANISM: Homo sapiens
62 (G) CELL TYPE: Fibroblast
63 (H) CELL LINE: WI-26 VA4
64
65 (vii) IMMEDIATE SOURCE:
66 (A) LIBRARY: WI-26 VA4
67 (B) CLONE: Clone 1
68
69 (ix) FEATURE:
70 (A) NAME/KEY: CDS
71 (B) LOCATION: 88..1473
72
73 (ix) FEATURE:
74 (A) NAME/KEY: mat_peptide
75 (B) LOCATION: 154..1470
76
77 (ix) FEATURE:
78 (A) NAME/KEY: sig_peptide
79 (B) LOCATION: 88..153
80
81
82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
83
84 GCGAGGCAGG CAGCCTGGAG AGAAGGCGCT GGGCTGCGAG GGCGCGAGGG CGCGAGGGCA 60
85
86 GGGGGCAACC GGACCCCGCC CGCATCC ATG GCG CCC GTC GCC GTC TGG GCC 111
87 Met Ala Pro Val Ala Val Trp Ala
88 -22 -20 -15
89
90 GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC 159
91 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
92 -10 -5 1
93
94 GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC 207
95 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
96 5 10 15
97
98 CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA 255
99 Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys

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	20	25	30	
100				
101				
102	TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC			303
103	Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp			
104	35 40 45 50			
105				
106	ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC			351
107	Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn			
108	55 60 65			
109				
110	TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG			399
111	Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln			
112	70 75 80			
113				
114	GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC			447
115	Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys			
116	85 90 95			
117				
118	AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG			495
119	Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu			
120	100 105 110			
121				
122	TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC AGA CCA			543
123	Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro			
124	115 120 125 130			
125				
126	GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG GGG ACG			591
127	Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr			
128	135 140 145			
129				
130	TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC CAG ATC			639
131	Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile			
132	150 155 160			
133				
134	TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC ATG GAT GCA GTC TGC			687
135	Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys			
136	165 170 175			
137				
138	ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA GGG GCA GTA CAC TTA			735
139	Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu			
140	180 185 190			
141				
142	CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG CAG CCA ACT CCA GAA			783
143	Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu			
144	195 200 205 210			
145				
146	CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC CCA ATG GGC CCC AGC			831
147	Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser			
148	215 220 225			
149				
150	CCC CCA GCT GAA GGG AGC ACT GGC GAC TTC GCT CTT CCA GTT GGA CTG			879
151	Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu			
152	230 235 240			

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153																		
154	ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC		927
155	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn		
156			245					250					255					
157																		
158	TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA		975
159	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg		
160		260					265					270						
161																		
162	GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG		1023
163	Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln		
164	275					280					285					290		
165																		
166	GGC	CCC	GAG	CAG	CAG	CAC	CTG	CTG	ATC	ACA	GCG	CCG	AGC	TCC	AGC	AGC		1071
167	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser		
168					295					300					305			
169																		
170	AGC	TCC	CTG	GAG	AGC	TCG	GCC	AGT	GCG	TTG	GAC	AGA	AGG	GCG	CCC	ACT		1119
171	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr		
172				310					315					320				
173																		
174	CGG	AAC	CAG	CCA	CAG	GCA	CCA	GGC	GTG	GAG	GCC	AGT	GGG	GCC	GGG	GAG		1167
175	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu		
176			325					330					335					
177																		
178	GCC	CGG	GCC	AGC	ACC	GGG	AGC	TCA	GAT	TCT	TCC	CCT	GGT	GGC	CAT	GGG		1215
179	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly		
180		340					345					350						
181																		
182	ACC	CAG	GTC	AAT	GTC	ACC	TGC	ATC	GTG	AAC	GTC	TGT	AGC	AGC	TCT	GAC		1263
183	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp		
184	355					360					365					370		
185																		
186	CAC	AGC	TCA	CAG	TGC	TCC	TCC	CAA	GCC	AGC	TCC	ACA	ATG	GGA	GAC	ACA		1311
187	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr		
188					375					380					385			
189																		
190	GAT	TCC	AGC	CCC	TCG	GAG	TCC	CCG	AAG	GAC	GAG	CAG	GTC	CCC	TTC	TCC		1359
191	Asp	Ser	Ser	Pro	Ser													

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206 TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCCC CCACCACTAG 1570
207
208 GACTCTGAGG CTCTTTCTGG GCCAAGTTCC TCTAGTGCCC TCCACAGCCG CAGCCTCCCT 1630
209
210 CTGACCTGCA G 1641
211
212

213 (2) INFORMATION FOR SEQ ID NO:2:
214

215 (i) SEQUENCE CHARACTERISTICS:

216 (A) LENGTH: 461 amino acids

217 (B) TYPE: amino acid

218 (D) TOPOLOGY: linear
219

220 (ii) MOLECULE TYPE: protein
221

222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
223

224 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
225 -22 -20 -15 -10
226
227 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
228 -5 1 5 10
229
230 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
231 15 20 25
232
233 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
234 30 35 40
235
236 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
237 45 50 55
238
239 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
240 60 65 70
241
242 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
243 75 80 85 90
244
245 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
246 95 100 105
247
248 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
249 110 115 120
250
251 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
252 125 130 135
253
254 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
255 140 145 150
256
257 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
258 155 160 165 170

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/385,229

DATE: 04/12/95
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Original Text